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PTO/SB/21 (08-00)

Approved for use through 10/31/2002. OMB 0651-0031

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TRANSMITTAL FORM

(to be used for all correspondence after initial filing)

Application Number	09/597,796
Filing Date	June 20, 2000
First Named Inventor	Skeiky, Yasir
Group Art Unit	1645
Examiner Name	Swartz, Rodney P.
Attorney Docket Number	014058-009050US

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Total Number of Pages in This Submission

39

ENCLOSURES (check all that apply)

- ☐ Fee Transmittal Form
 - ☐ Fee Attached
- ☐ Amendment / Reply
 - ☐ After Final
 - ☐ Affidavits/declaration(s)
- ☐ Extension of Time Request
- ☐ Express Abandonment Request
- ☐ Information Disclosure Statement
- ☐ Certified Copy of Priority Document(s)
- ☐ Response to Missing Parts/Incomplete Application
 - ☐ Response to Missing Parts under 37 CFR 1.52 or 1.53

- ☐ Assignment Papers (for an Application)
- ☐ Drawing(s)
- ☐ Licensing-related Papers
- ☐ Petition
- ☐ Petition to Convert to a Provisional Application
- ☐ Power of Attorney, Revocation Change of Correspondence Address
- ☐ Terminal Disclaimer
- ☐ Request for Refund
- ☐ CD, Number of CD(s)

- ☐ After Allowance Communication to Group
- ☐ Appeal Communication to Board of Appeals and Interferences
- ☐ Appeal Communication to Group (Appeal Notice, Brief, Reply Brief)
- ☐ Proprietary Information
- ☐ Status Letter
- ☒ Other Enclosure(s) (please identify below):
Return Postcard; Communication Under 37 CFR 1.821-1.825 and Amendment; disk containing sequence listing; copy of Notice to Comply..

Remarks

The Commissioner is authorized to charge any additional fees to Deposit Account 20-1430.

SIGNATURE OF APPLICANT, ATTORNEY, OR AGENT

Firm and Individual name	Townsend and Townsend and Crew LLP	Reg. No. 42,058
Signature		
Date	December 4, 2002	

CERTIFICATE OF MAILING

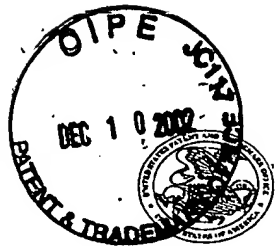
I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: Commissioner for Patents, Washington, D.C. 20231 on this date:

US Patent & Trademark Office, Box Sequence, 12/04/02
P.O. Box 2327, Arlington, VA 22202 on this date

Typed or printed name	Dana Kane	Date	12/04/02
Signature			

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SF 1412252 v1



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ASP/UA

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/597,796	06/20/2000	Yasir Skeiky	014058-009050US	6269

20350 7590 11/04/2002

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EIGHTH FLOOR
SAN FRANCISCO, CA 94111-3834

EXAMINER

SWARTZ, RODNEY P

ART UNIT PAPER NUMBER

1645

DATE MAILED: 11/04/2002

15

Response Due SCR. LIST. 12/4/02 ALB

Please find below and/or attached an Office communication concerning this application or proceeding.



UNITED STATES DEPARTMENT OF COMMERCE
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Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/597,796			

EXAMINER	
Rodney P. Swartz, Ph.D.	
ART UNIT	PAPER NUMBER
1645	

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application
Commissioner of Patents

This Application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR §§ 1.821 - 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequences And/Or Amino Acid Sequence Disclosures.

Any inquiry concerning this communication should be directed to Examiner Rodney P. Swartz, Ph.D., Art Unit 1645, whose telephone number is (703) 308-4244. If unable to reach the examiner, Lynette Smith, SPE, can be contacted at (703) 308-3909.

Any questions regarding compliance with the sequence rules requirements specifically should be directed to the departments listed at the bottom of the Notice To Comply.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

APPLICANT IS GIVEN ONE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.F.R. §§ 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Rodney P. Swartz, Ph.D.
November 4, 2002



Application No. 09/597,796

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CAR §1.821 - §1.825 for the following reasons(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 CAR §1.821 - §1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990, and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CAR §1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CAR §1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CAR §1.822 and/or §1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing".
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CAR §1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CAR §1.821(e).
- ☐ 7. Other: _____

APPLICANT MUST PROVIDE:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as were as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CAR §1.821(e) or §1.821(f) or §1.821(g) or §1.825(b) or §1.825(d).

FOR QUESTIONS REGARDING COMPLIANCE WITH THESE REQUIREMENTS, PLEASE CONTACT:

For Rules Interpretation, call (703) 308-1123
For CRF Submission help, call (703)308-4212
For Patentin Software help, call (703) 557-0400

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE.

ERROR DETECTED**SUGGESTED CORRECTION**SERIAL NUMBER: 09/597,796B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO S

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading).
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X°(insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

1600

RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/09/597,796B

TIME: 12:32:10

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Output Set: N:\CRF3\01152002\I597796B.raw

Does Not Comply
Corrected Diskette Needed

PP 3, 6-8

3 <110> APPLICANT: Skeiky, Yasir
 4 Reed, Steven
 5 Alderson, Mark
 6 Corixa Corporation
 8 <120> TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
 10 <130> FILE REFERENCE: 014058-009050US
 12 <140> CURRENT APPLICATION NUMBER: US 09/597,796B
 13 <141> CURRENT FILING DATE: 2001-06-20
 15 <150> PRIOR APPLICATION NUMBER: US 09/056,556
 16 <151> PRIOR FILING DATE: 1998-04-07
 18 <150> PRIOR APPLICATION NUMBER: US 09/223,040
 19 <151> PRIOR FILING DATE: 1998-12-30
 21 <150> PRIOR APPLICATION NUMBER: WO PCT/US99/07717
 22 <151> PRIOR FILING DATE: 1999-04-07
 24 <150> PRIOR APPLICATION NUMBER: US 09/287,849
 25 <151> PRIOR FILING DATE: 1999-04-07
 27 <150> PRIOR APPLICATION NUMBER: US 60/158,338
 28 <151> PRIOR FILING DATE: 1999-10-07
 30 <150> PRIOR APPLICATION NUMBER: US 60/158,425
 31 <151> PRIOR FILING DATE: 1999-10-07
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 38 <211> LENGTH: 588
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Mycobacterium tuberculosis
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 43 <223> OTHER INFORMATION: Ra35, N-terminus of MTB32A (TbRa35FL)
 45 <220> FEATURE:
 46 <221> NAME/KEY: CDS
 47 <222> LOCATION: (1)..(588)
 48 <223> OTHER INFORMATION: Ra35
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 64 <211> LENGTH: 195
 65 <212> TYPE: PRT
 66 <213> ORGANISM: Mycobacterium tuberculosis

RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/09/597,796B

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70 <400> SEQUENCE: 2

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74           20           25           30
75 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
76           35           40           45
77 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
78           50           55           60
79 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
80   65           70           75           80
81 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
82           85           90           95
83 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
84           100          105          110
85 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
86           115          120          125
87 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
88           130          135          140
89 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
90   145          150          155          160
91 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
92           165          170          175
93 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
94           180          185          190
95 Ala Ala Ser
96           195

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99 <210> SEQ ID NO: 3

100 <211> LENGTH: 1872

101 <212> TYPE: DNA

102 <213> ORGANISM: Mycobacterium tuberculosis

104 <220> FEATURE:

105 <223> OTHER INFORMATION: MTB32A (TbRa35FL) cDNA

107 <400> SEQUENCE: 3

P.3

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119 gacattgaac gggttgatcc agttcgatgc cgcaatccag cccggtgatt cgggcggggc 720
120 cgtcgtcaac ggcctaggac aggtggtcgg tatgaacacg gccgcgtccg ataacttcca 780
121 gctgtcccg ggtgggcagg gattcgccat tccgatcggg caggcgatgg cgatcgcggg 840

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RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/09/597,796B

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 133 tggcttgga tcgactgat ctgttgccgc cgttcctacg actcaccgct gcgcgacggc 1560
 134 ggttacgaca ttcgcgactt ctacaagggt ctgcccgaat tcggcaccgt cgacgatttc 1620
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 137 tacggtgact attacgtgtg gacgcacacc agcgcgcgt acaccgacgc ccggatcatc 1800
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 139 gcaccgattc tt 1872
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 143 <211> LENGTH: 355
 144 <212> TYPE: PRT
 145 <213> ORGANISM: Mycobacterium tuberculosis
 147 <220> FEATURE:
 148 <223> OTHER INFORMATION: MTB32A (TbRa35FL) protein
 150 <400> SEQUENCE: 4
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 154 20 25 30
 155 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 156 35 40 45
 157 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 158 50 55 60
 159 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 160 65 70 75 80
 161 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 162 85 90 95
 163 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 164 100 105 110
 165 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 166 115 120 125
 167 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 168 130 135 140
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 170 145 150 155 160
 171 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 172 165 170 175
 173 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 174 180 185 190

see
 item 9
 on
 Error
 Summary
 Sheet

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DATE: 01/15/2002

PATENT APPLICATION: US/09/597,796B

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178      210      215      220
179 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
180 225      230      235      240
181 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
182      245      250      255
183 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
184      260      265      270
185 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
186      275      280      285
187 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
188      290      295      300
189 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
190 305      310      315      320
191 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
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195 Pro Pro Ala

196 355

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201 <212> TYPE: DNA

202 <213> ORGANISM: Mycobacterium tuberculosis

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205 <223> OTHER INFORMATION: MTBRa12 C-terminus of MTB32A (Ra35FL)

207 <400> SEQUENCE: 5

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220 <212> TYPE: PRT

221 <213> ORGANISM: Mycobacterium tuberculosis

223 <220> FEATURE:

224 <223> OTHER INFORMATION: MTBRa12 C-terminus of MTB32A (Ra35FL)

226 <400> SEQUENCE: 6

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RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/09/597,796B

TIME: 12:32:10

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Output Set: N:\CRF3\01152002\I597796B.raw

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234          50          55          60
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236 65          70          75          80
237 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
238          85          90          95
239 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
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249 <212> TYPE: DNA
250 <213> ORGANISM: Mycobacterium tuberculosis
252 <220> FEATURE:
253 <223> OTHER INFORMATION: MTB39 (TbH9) cDNA full-length
255 <400> SEQUENCE: 7
256 gatcgtagcc gtgcgagtgc tcgggcccgtt tgaggatgga gtgcacgtgt ctttcgtgat 60
257 ggcataccca gagatgttgg cggcgccggc tgacaccctg cagagcatcg gtgctaccac 120
258 tgtggctagc aatgccgctg cggcgccccc gacgactggg gtggtgcccc ccgctgccga 180
259 tgagggtgctg gcgctgactg cggcgcaactt cgccgcacat gcggcgatgt atcagtccgt 240
260 gacgctcggg gctgctgcga ttcattacca gtctgtggcc acccttgcca gcagcgccag 300
261 ctctgtatgcg gccactgaag tcgccaatgc ggcggcggcc agctaagcca ggaacagtcg 360
262 gcacgagaaa ccacgagaaa tagggacacg taatggtgga tttcggggcg ttaccaccgg 420
263 agatcaactc cgcgaggatg tacgccggcc cgggttcggc ctctgtggtg gccgcggctc 480
264 agatgtggga cagcgtggcg agtgacctgt tttcgcccg ctcggcggtt cagtcggttg 540
265 tctggggctc gacggtgggg tcgtggatag gtctgtcggc gggctctgat gtggcgccgg 600
266 cctcgccgta tgtggcgtgg atgagcgtca ccgcggggca ggccgagctg accgcgcgcc 660
267 aggtccgggt tgctgcggcg gcctacgaga cggcgatagg gctgacggtg ccccgccggg 720
268 tgatcgccga gaaccgtgct gaactgatga ttctgatagc gaccaacctc ttggggcaaa 780
269 acaccccggc gatcgcggtc aacgaggccg aatacggcga gatgtgggcc caagacgccg 840
270 ccgcgatggt tggtacgcc gcggcgacgg cgacggcgac ggcgacgttg ctgccgttcg 900
271 aggaggcgcc ggagatgacc agcgcggtg ggctcctcga gcaggccgcc gcggtcgagg 960
272 aggcctccga caccgcgcg gcgaaccagt tgatgaacaa tgtgccccag gcgctgcaac 1020
273 agctggccca gccacgcag ggcaccacgc cttcttccaa gctgggtggc ctgtggaaga 1080
274 cggctctgcc gcatcggtcg ccgatcagca acatggtgtc gatggccaac aaccacatgt 1140
275 cgatgaccaa ctcggtgtg tcgatgacca acacctgag ctcgatgttg aagggtttg 1200
276 ctccggcggc ggccgcccag gccgtgcaaa ccgcggcgca aaacggggtc cgggcgatga 1260
277 gctcgtggtg cagctcgtg ggttcttcgg gtctggcgcg tggggtggcc gccaaacttg 1320
278 gtcgggcggc ctcggtcggt tcgttgctcg tgccgcaggc ctgggcccgc gccaccagg 1380
279 cagtcacccc ggcggcgcg gcgctgccgc tgaccagcct gaccagcgcc gcggaaagag 1440
280 ggcccgggca gatgctgggc gggctgccgc tggggcagat gggcgccagg gccggtggtg 1500
281 ggctcagtg tgtgctgct gtccgcgcgc gacctatgt gatgccgat tctccggcg 1560
282 ccggttagga gagggggcg agactgtcgt tatttgacca gtgatcgcg gtctcggtgt 1620
283 ttccgcggcc ggctatgaca acagtcaatg tgcattgaaa gttacaggtg ttaggtccag 1680
284 gttcaacaag gagacaggca acatggctc acgttttatg acggatccgc acgcgatgcg 1740

```

04,597,796B 6

<210> 10

<211> 596

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: fusion
protein TbH9-Ra35 (MTB59F)

<400> 10

> <220> Insert this
mandatory
numeric identifier
wherever <221>, <222>
or <223> is
shown
↓

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

<210> 11
 <211> 2287
 <212> DNA
 <213> Mycobacterium tuberculosis
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: fusion
 protein Ra12-TbH9-Ra35 (MTB72F)

<213> can only have one response:

Artificial Sequence
or Unknown or
 Scientific name
 (Genus/species)

<210> 25
<211> 851
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB39 (TbH9) cDNA

<400> 25
ctgcagggtg gcgtggatga gcgtcaccgc ggggcaggcc gagctgaccg ccgcccaggt 60
ccgggttgct gcggcgccct acgagacggc gtatgggctg acggtgcccc cgccggtgat 120
cgccgagAAC cgtgctgaac tgatgattct gatagcgacc aacctcttgg ggcaaaacac 180
cccggcgatc gcggtcaacg aggccgaata cggcgagatg tgggcccagg acgcccggcg 240
gatgtttggc tacgcccgcg cgacggcgac ggcgacggcg acgttgctgc cgttcgagga 300
ggcgccggag atgaccagcg cgggtgggct cctcgagcag gccgccggcg tcgaggaggc 360
ctccgacacc gccgcggcga accagttgat gaacaatgtg ccccgaggcg tgaaacagtt 420
ggcccagccc acgcagggca ccacgccttc ttccaagctg ggtggcctgt ggaagacggt 480
ctcgccgcat cggctgcgca tcagcaacat ggtgtcgatg gccacaacc acatgtcgat 540
gaccaactcg ggtgtgtcga tgaccaaacac cttgagctcg atgttgaagg gctttgctcc 600
ggcggcgggc gcccaggccg tgcaaacccg ggcgcaaaac ggggtccggg cgatgagctc 660
gctgggcagc tcgctgggtt cttcggtgtc ggcgggtggg gtggccgcca acttgggtcg 720
ggcggcctcg gtacggtatg gtcaccggga tggcggaata tatgcaggt ctggtcggcg 780
gaacggtggt ccggcgtaag gtttaccgcc gttttctgga tgcggtgaac ttcgtcaacg 840
gaaacagtta c 851

see
item 9
on Enon
Summary
Sheet

IMPORTANT
→

Use of n or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/597,796B

DATE: 01/15/2002

TIME: 12:32:11

Input Set : A:\-90-5.app

Output Set: N:\CRF3\01152002\I597796B.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:132 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
 L:132 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
 L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
 L:138 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
 L:138 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
 L:138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
 L:421 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:508 M:280 W: Numeric Identifier already exists, Organism not replaced.
 L:535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
 L:572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
 L:580 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:804 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:1082 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
 L:1082 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
 L:1082 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
 L:1126 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
 L:1126 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
 L:1126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
 L:1181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27